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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    earched:
                                                                                                                                                                                                                                            SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671580 seqs, 206047115 residues
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3615
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                                                                                  sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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sp_human:*
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sp_organelle:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match 1	% Query Match Length DB	В	ID	Description
_	1353	37.4	653	12	Q64906	Q64906 alcelaphine
2	810.5	22.4	612	12	Q9J5F6	Q9j5f6 fowlpox vir
ω	680.5	18.8	893	4	Q9С0В8	Q9c0b8 homo sapien
4	617.5	17.1	748	4	Q8TB71	Q8tb71 homo sapien
σ	601.5	16.6	754	4	Q8TDV7	Q8tdv7 homo sapien
6	597	16.5	756	13	080009	Q8qgu9 gallus gall
7	596.5	16.5	635	4	Q96GX0	Q96gx0 homo sapien
8	566	15.7	775	11	Q9QX23	Q9qx23 mus musculu
9	534	14.8	782	4	Q9NS98	Q9ns98 homo sapien
10	516	14.3	761	4	Q8WUA9	Q8wua9 homo sapien
11	500.5	13.8	963	4	Q9C0C4	Q9c0c4 homo sapien
12	444.5	12.3	1049	4	Q9P2H9	Q9p2h9 homo sapien
13	437	12.1	1030	4	Q9H2E6	Q9h2e6 homo sapien
14	426.5	11.8	296	11	Q9JI29	Q9ji29 rattus norv
15	418	11.6	1202	4	Q9P283	Q9p283 homo sapien
16	407	11.3	724	σ	Q9V7Q7	Q9v7q7 drosophila

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
215	224.5	230	236	236.5	236.5	246	248.5	267.5	276.5	304.5	309.5	310.5	311	312	337	349.5	360.5	368	373.5	380.5	380.5	387	389	389	392.5	393.5	397.5	402
5.9	6.2	6.4	6.5	6.5	6.5	6.8	6.9	7.4	7.6	8.4	8.6	8.6	8.6	8.6	9.3	9.7	10.0	10.2	10.3	10.5	10.5	10.7	10.8	10.8	10.9	10.9	11.0	11.1
1892	1944	228	1951	2051	816	424	510	284	367	1081	1083	458	475	676	418	457	920	416	923	687	409	770	935	770	963	1022	616	1005
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Q9QY40	Q9N375	Q9JF56	Q8TA58	096682	Q9V4A7	Q9NS35	Q9NX92	054948	09нан9	Q9U631	Q9VTT0	Q8WVP9	Q96FK5	Q9TYS4	Q96JU9	Q9HBR1	Q8R4U4	Q98VP6	Q8R4U3	Q9BXR8	Q8QMR4	Q9V3M4	Q96JF8	044253	Q91Y36	Q9P249	Q9V7P8	Q9EQ71
Q9qy40 mus musculu	Q9n375 caenorhabdi	Q9jf56 vaccinia vi	Q8ta58 caenorhabdi	096682 drosophila	Q9v4a7 drosophila	Q9ns35 homo sapien	Q9nx92 homo sapien	O54948 mus musculu	Q9hah9 homo sapien	Q9u631 drosophila	Q9vtt0 drosophila		Q96fk5 homo sapien			Q9hbrl homo sapien	Q8r4u4 rattus norv	Q98vp6 vaccinia vi	Q8r4u3 mus musculu	Q9bxr8 homo sapien	Q8qmr4 cowpox viru	Q9v3m4 drosophila	Q96jf8 homo sapien	044253 drosophila	6 mus	Q9p249 homo sapien	Q9v7p8 drosophila	Q9eq71 mus musculu

ALIGNMENTS

	SC	DH	DF	DF	RI	R₽	RC	RF	RN	RI	RI	R₽	RX	RC	RF	RN	RI	RI	R₽	RX	RC	RE	RN	ΚO	8	8	SO	DE	ᄗ	멁	DI	AC	II	Q R Q E	,
Query Match 37.4%; Score 1353; DB 12; Length 653; Best Local Similarity 45.9%; Pred. No. 5.6e-106;	DR PIAM; PF01403; Sema; 1. SQ SEQUENCE 653 AA; 73645 MW; 5C2816BD567E706E CRC64;	InterPro; IPR001627;			Submitted (MAY-1997) 1		RC STRAIN=C500;	RP SEQUENCE FROM N.A.	RN [3]	. 71:6517-6525(1997).	"Primary structure of the alcelaphi		MEDLINE=97404659; Publ	STRAIN-C	RP SEQUENCE FROM N.A.	[2	J. Gen. Virol. 76:1063-1067(1995).	RT "Alcelaphine herpesvirus type 1 has a semaphorin-like gene.";	Ensser A., Fleckenstein B.;	RX MEDLINE=97201573; PubMed=9049359;	RC STRAIN=C500;	RP SEQUENCE FROM N.A.		OX NCBI_TaxID=35252;	Gammaherpesvirinae; Rhadinovirus.	Viruses; dsDNA viruses, no RNA stage; Herpesvirida	Alcelaphine herpesvirus 1 (wildebeest	Similar to GENBANK ACCE:	01-JUN-2001 (TrEMBLrel. 17, Last annotation	(TrEMBLrel. 01,	01-NOV-1996 (TrEMBLrel.	Q64906;	ID Q64906 PRELIMINARY; PRT; 653 AA.	RESULT 1 Q64906	

Matches

24;

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09J5F6;
09J5F6;
01-OCT-2000
01-OCT-2000
01-JUN-2002
0RF FPV047 s
                                                                                   "The y.
"Virol.
                                                         SEQUENCE
Afonso C.
Afonso C.L., Tulman E.R., Lu Z., Zs
Submitted (OCT-1999) to the EMBL/Ge
EMBL; AF198100; AAF44391.1; -
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
                                                                                                                             Afonso
                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=20193820; PubMed=10729156;
                                                                                                                                                                                    Avipoxvirus.
NCBI_TaxID=10261;
                                                                                                                                                                                                               Viruses; dsDNA
                                                                                                                                                                                                                              Fowlpox virus
                                                                                                so C.L., Tulman E.R., Lu Z., genome of fowlpox virus."; irol. 74:3815-3831(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNKNENRLQDVFLLPDPSGQWRDTR
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 21, Last annotation
semaphorin vaccinia A39R homolog.
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EMBL/GenBank/DDBJ
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Best Local Sim
Matches 199;
                                                                                                                          Q9C0B8 PRELIMINARY;
Q9C0B8;
Q1-JUN-2001 (TrEMBLrel. 17, C
Q1-JUN-2002 (TrEMBLrel. 17, L
Q1-JUN-2002 (TrEMBLrel. 21, L
KIAA1745 protein (Fragment).
KIAA1745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001627; Sem Pfam; PF01403; PSI; 1. Pfam; PF01403; Sema; 1. SMART; SM00423; PSI; 1. SEQUENCE 612 AA; 6951
SEQUENCE FROM N.A. MEDLINE=21082932; P. Nagase T., Kikuno R. "Prediction of the
                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                      566
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                                                                                                                                                                                                                                                                                                                                             VNKHNKTIVDCGPDN-NDMCYFFIYNLYDDNFGKYTCTSEEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFRTSSLKGYH-SSLPNPRPGKCLPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLFH 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQYPSPVLALVSDERSEKLFVSYNDSTIELPLAFCHLYGGTCDSCLLSRDPHCGWTNIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKYTYTHIVINTAVINYQHKDYRVTTFYLSTSDGKIHKVVVYEDG------VINVIELTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKYHYQKVAVHRMQASHGETFH---VLYLTTDRGTIHKVV--EPGEQEHSFAFNIMEIQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRV----KSKLTENNIEFRYKTYMEDVVIYRTDCNTRLIIGVTNTVYVVNTTDKSNITVD
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Metazoa; Chordata; C
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              Hattori
sequences
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98; Pred. No. 5.3e-60;
108; Mismatches 224
                                                                                                                                                      Created)
Last sequence
Last annotation
                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                 PRT;
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                                                                                                                                                     sequence update)
annotation update)
             Kondo
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 o Y., Okumura
unidentified
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                                                                                    Hominidae;
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Ohara O.;
an genes.
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RESULT Q9J5F6

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Euteleostomi;

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Best Loc
Matches
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InterPro: IPR002165; Plexin_repeat.
InterPro: IPR001627; Sema.
Pfam; PF01437; PSI; 1.
Pfam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
NON_TER
  Q8TB71
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Res. 7:347-355(2000).
L; AB051532; BAB21836.1;
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                                                                                                                                                                                                                                                                                                                                                    THPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVRSRMLLLQP----
                                                                                                                                                                                                                                                                                                                                                                                                     LSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVNRETQQWYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEFEFFENTIVSRIARICKGDEGGERVLQ-QRWTSFLKAQLLCSRPDDGFPFNVLQDVFT
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                                                                                                QHWQLLPEDGI 635
                                                                                                                                                                                                                                         GQPVQNLLLDTHRGLLYAASHSGVVQVPMANCSLY-RSCGDCLLARDPYCAWSGSSCKHV
                                                                                                                                                                                                                                                                  AAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRC--I
                                                                                                                                                                                                                                                                                                              HSSLPNPRPGKCLPD--QQPIPTETFQVADR------HPEVAQRVEPMGPLKTPL
                                                                                                                                                                                                                                                                                                                                                                                                                          LPDPSGQWRDTRVYGVFSNPWNY-----SAVCVYSLGDIDKVF------RTSSLKGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPVSPAEPPEPEPRDTVAPALRMLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPP
                                                                       SYCPEVVEDGV
                                                                                                                          LSNLATRLWLRNGAPVNASASC---HVLPTGDLLL--VGTQQLGEFQCWSLEEGFQQLVA
                                                                                                                                                    ESRHATYSWRHK---ENVEQSCEPGHQSPNCILFIENLTAQQYGHYFC-EAQEGSYFREA
                                                                                                                                                                                SLYQPQLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPL
                                                                                                                                                                                                          SIYSSE---RSVLQSINPAEPHKEC-----PNPKP-DKAPLQKVSLAPNSRYYLSCPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTNARHPSCW--NLVNGTV------VPLGEMRGYAPFSPDENSLVLFEGDEVYSTIRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKGKDPQRDCQNYIKILLPLSGSHLFTC
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  PRELIMINARY;
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01-JUN-2002 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Hypothetical 83.0 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                              QSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHL 640
                                                                                                          TLCSGDSSRPALLEHKVFGVEGSSAFLECEPRSLQARVEWTFQRAGVTAHTQVLAEERTE
                                                                                                                                    KECPNPKPDKAPLQ-KVSLAPNSRYYLSCPMESRHATYSWRH
                                                                                                                                                                                                                                         TFHVLYLTTDRGTIHKV--VEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVS : ||:: | :||::|: :| :||:
                                                                                                                                                                                                                                                                              TFSSTKDFPDDVIQFARNHPLMYNSVLPTG--GRPLFLQVGANYTFTQIAADRVAAADGH
                                                                                                                                                                                                                                                                                                                                                              VFSNP--WNYSAVCVYSLGDIDKVF------RTSSLKGYHSSLPNPRPGKC-----
                                                                                                                                                                                                                                                                                                                                                                                       CRGDQGGESSLSVSKWNTFLKAMLVCS--DAATNKNFNRLQDVFLLPDPSGQWRDTRVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLRTEPHDSRWLNEPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELYT----SDTVMQNPQFIKA-TIVHQDQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQL
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                                                      RTARG
                                                                                                                                                                SRSAVAQIALHRCAAHGRVCTECCLARDPYCAWDGVACTRFQPSAKRRFRRQDVRNGDPS
                                                                                                                                                                                            SQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSS--ERSVLQSINPAEPH
                                                                                                                                                                                                                        -YDVLFIGTDVGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMQISSKRHQLYVA
                                                                                                                                                                                                                                                                                              -LPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLF---HSKYHYQKVAVHRMQASHGE : | : | | : | | : | : | : |
                                                                                                                                                                                                                                                                                                                                     VFSTSSIFQGSAVCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRPGMCPSKTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EECNWAGKDIGT-----ECMNFVKLLHAYNRTHLLACGTGAFHPTC-----AFVEVGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GSTKGSCLDKRDCENYITLLERRSE-GLLACGTNARHPSCWNLVNGTVVPLG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEEPVLRLDPGRIEDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRP
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                                                      LLLRRLRRRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERL
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28.2%;
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Pred. No. 1.7e
92; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
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·--KENVE

584 562 480 443

502

323

268 265 208

325

385

366

148 164 99 113 42

210

670

.7e-43; DΒ 293;

Indels Length

129;

Gaps

27;

62

4:

CRC64;

databases

Koyama

Query Match Best Local Matches

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"semaphorin 3B (SEMA3B) cDNA.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB083186; BAB88870.1;
SEQUENCE 754 AA; 83691 MW; E61FD08C04E9A68E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                          386 PSKTFGTFSSTKDFPDDVIQFARNHPLMYNSVLPTG--GRPLFLQVGANYTFTQIAADRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GRAAPSAPRARVPGPPARLGLPLRLLLLLWA----AAASAQGHLRSGPRIFAVWKGHV
                                                                                                                                                                                                                                                                                AEERTERTARG - -
                                                                                                                               RNGDPSTLCSGDSSRPALLEHKVFGVEGSSAFLECEPRSLQARVEWTFQRAGVTAHTQVL
                                                                                                                                                                                                                                RKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSS--ERSVLQSI
                                                                                                                                                                                                                                                                                                                                                                               -----LPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLF---HSKYHYQKVAVHRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRVYGVFSNP---WNYSAVCVYSLGDIDKVF-----RTSSLKGYHSSLPNPRPGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRGDQGGESSLSVSKWNTFLKAMLVCS--DAATNKNENRL----QDVFLLPDPSGQWRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GSTKGSCLDKRDCENYITLLERRSE-GLLACGTNARHPSCWNLVNGTVVPLG---
                                                                                                                                                                  NPAEPHKECPNPKPDKAPLQ-KVSLAPNSRYYLSCPMESRHATYSWRH----
                                                                                                                                                                                                                                                                                                                       QASHGETFHVLYLTTDRGTIHKV--VEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAER
                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLYAVESTSSSIFQGSAVCVYSMNDVRRAFLGPEAHKEGPMHQWVSYQGRVPYPRPGMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRTEPHDSRWLNEPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELYT - - - SDTVMQNPQFIKA-TIVHQDQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEEPVLRLDPGRIEDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EECNWAGKDIGT-----ECMNFVKLLHAYNRTHLLACGTGAFHPTC-----AFVEVGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLQTFSLERTCCYQALLVDEERGRLFVGAENHVASLNL---DNISKRAKKLAWPAPVEWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRAGAAAV---IPG-----LALLWAVGLGSAAPSPPRLRLSFQELQAWH---
                                                                                          -KENVEQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAE
                                                                                                                                                                                                          HQLYVASRSAVAQIALHRCAAHGRVCTECCLARDPYCAWDGVACTRFQPSAKRRFRRQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRNDVGGQRSL-VNKWTTFLKARLVCSVPGVEGDTHFDQLRPFPAEDVFLL--SSRDHRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNI------
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01; Conservative
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27.8%;
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                                                        LLLRRLRRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
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3; Mismatches 293;
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Best Local
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O8OGU9;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AB072930; BAB88691.1; -. SEQUENCE 756 AA; 85196 MW; C36754C02541ED88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Axon guidance of the boundary.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Watanabe Y., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEMA3F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ma
Local 202;
 592
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                   YLSCPMESRHATYSW-RHKENVEQSCEPGHQSPNCI-----LFIENLTAQQYGHYFCEAQ
FLECOPRSPOATVKWLLQKDNSDRRKELRTEGGRALRTEQGLLLRALQLSDSGLYSCTAT
                                                                                            PYCGWDQGRCISIYSS---ERSVLQSINPAEPHKECP--NPKPDKAPLQKVSL-APNSRY
                                                                                                                                                                        FAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRD
                                                                                                                                                                                                                                               PMGPLKTPLF---HSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKV-VEPGEQEHS
                                                                                                                                                                                                                                                                                                                                                                             IETHFDELQDVFI-----QQTQDTKNPVIYAVFSASGSVFKGSAVCVYSMADIRMVFNRP
                                                                                                                                                                                                                                                                                                                                                                                                      TNKNFNRLQDVFLLPDPSGQWRDTR----VYGVFS----NPWNYSAVCVYSLGDIDKVFRT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFFREDNPDKNPEAPLN---VSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS---DAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYAGV-YIDFMGTDAAIFRTMGKQTAMRTDQYNSRWLNDPAFVRAQLIPDSSERNDDKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGSKDYVLSLDLHDINREPLIIHWPASQQRIEECILSGKNS---NGECGNFIRLIQPWNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGGRGKVYLFDFPEGKN------ASVRTVN--IGSTKGSCLDKRDCENYITLLE--RR 136
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                                                                         PYCAWD-GKACSRYSASSKRRSRRQDVRHGNPMRQCRGYNSNANKNTVEAVQYGVEGSTA
                                                                                                                                                  EELMLEETEVFKVPAPIKMMTISSKRQQLYVSSAVGVTHLALHRCDVYGEACADCCLARD
                                                                                                                                                                                                                                                                                                   FAHKEGPNYQWMPYTGKMPYPRPGTCPGGTFTPSMKSTKDYPDEVINFMRSHPLMYHAVY
                                                                                                                                                                                                                                                                                                                         -SSLKG-----YHSSLPNPRPGKC------LPDQQPIPTETFQVADRHPEVAQRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFFRE----KSADAPLSPGVYSRIGRICLNDDGGHCCL-VNKWSTFLKARLVCSVPGPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYSTIRKQEYNGKIPRERRIRGESELYTSDTV----MQNPQFIKATIV-HQDQAYDDKIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TH-LYVCGTGAYNPICAFINRGRKAQDYIFYLEPDKLESGKGKCSYDPKVDTVSALINEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGLLACGTNARHPSCWNLVNGTVV-----PLGEMRGYAPFSPDENSLVLFEGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLTLGWRAAHGKDG-VPPTPRVQLSFKELKATGTAHFFNFLLNSSDYRILLKDEDHDRMY
                                                                                                                                                                                                                            PAH~-RQPLVVRTNVNYRFTTIAVDQVDAADGR-YEVLFLGTDRGTVQKVIVLPRDDMET
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trochlear nerve
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21,
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; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Matches 175
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
Unknown (protein for MGC:18122)
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 1g; 1. Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; BC009113; AAH09113.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001627; Sema.
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Mammalia; Eutheria;
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                                               YFCEAQEGSYFREAQHWQLLPEDGIMAEHL 640
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  YLCAAVEQGFTQPLRRLSLHVLSATQAERL
                                                                                            LECEPRSLQARVEWTFQRAGVTAHTQVLAEERTERTARG
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30.7%; pred. No. 7.9e-42;
cive 79; Mismatches 245
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RESULT 8
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ID Q9QX23
AC Q9QX23
AC Q9QX23
DT Q1-MAY-
DX SEQUENC
C Mammali
OX NCBI_TA
RN [1]
RP SEQUENC
RT SEQUENC
RT ALINE
RA Miyazak
RT A nove
RT A nove
RT SEQUENC
RT EMBL; A
DR MGD; MG
DR InterPr
DR SMART;
SQ SEQUENC
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Best Local Similarity
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003659; Plexin-like
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01-MAY-2000
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                                                                         VCSDAATN---KNENRLQDVFLLP--DPSGQWRDTRVYGVF---SNPWNYSAVCVYSLGD
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Metazoa; Chordata; C
---haria; Rodentia; f
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Pred. No. 4.1e-39;
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RESULT 9
Q9NS98
ID Q9NS
AC Q9NS
DT 01-C
DT 01-J
DE Sema
GN SEM2
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                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                InterPro; IPR001627; Sema. Pfam; PF00047; ig; 1 Pfam; PF01403; Sema; 1 SMART; SM00409; IG; 1 SMART; SM00410; IG_like; 1 SMART; SM00423; PSI; 1 SMART; SM00423; PSI; 1 ...
                                                                                                                                                                                                                                                        SMART; SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Semaphorin sem2 (FLJ00014 protein).
SEM2 OR FLJ00014.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2000) to the EMEMBL; AB029496; BAA98132.1; -. EMBL; AK024425; BAB15715.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86SN60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seki N., Hattori A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9NS98; Q9H7Q3;
                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                        spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohara O., Nagase T., Kiku
"The nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                               [nterPro;
 152
                         164
                                                  102
                                                                          110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human semaphorin.";
                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE OF 58-782 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                           59
                                                                                                                                                     24
                                                                                                                                                                            4
                                                                                                                                                                            PPPGRAAPSAPRARVPGPPARLGLPLRLLLLLLWAAAASA-----QGHLRSGPRIFAVW 58
                                                                          TVNIGSTKGSCLDK - - - - -
                                                                                                                                                     PSPG---PSVPRLR-----LSYRDLL---SANRSAIFLGPQGSLNLQAMYLDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIENLTAQQYGHYFCEAQEGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CADCCLARDPYCAWDGISCSRYYPTGAHAKRRFRRQDVRHGNAAQQCFGQQFVGDALDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHGCLMSRDPYCGWDQGRCISIY-----SSERSVLQSINPAEPHKECPNPK--PDKAPLQ
 GEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYTGL-TADFLGREAMIFRSGGPRP
                                                                                                                           KGHV---GQD-----RVDFGQTEPHTVLF-HEPGSSSVWVGGRGKVYLFDFPEGKNASVR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFL-RVRKSDAGTYFCQTVEHNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVSLA---PNSRYYLSCPMESRHATYSW-----RHKENVEQ-----SCEPGHQSPNCI
                                                                                                   RDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EERLAYGIESNSTLLECTPRSLQAKVIWFVQKGRDVRKEEVKTDDRVVKMDLG---
                                                                                                                                                                                                       194;
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                            IPR003599; Ig.
IPR003600; Ig_like.
IPR003006; Ig_MHC.
IPR003659; Plexin-like.
                                                 REECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALI--
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                       86700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kikuno
lence of
                      RGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESE
                                                                                                                                                                                                                  14:88;
27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi
                                                               RDCENYITLLERRSE-GLLACGTNARHPSCWNLVNGTVVPL 163
                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                R., Okumura
a long cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                   Score 534; DB 4;
Pred. No. 2.2e-36;
3; Mismatches 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620
                                                                                                                                                                                                                                                        85CB424874DF6663 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kozuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       782
                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.;
clone
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                                                                                                                                                                                                      260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muramatsu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                           databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                            Length
                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
                                                                                                                                                                                                      162;
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                                                 -TVGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                    Gaps
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Q8WUA9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                                                                                                                                                Query Match
Best Local S
Matches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WUA9;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                      PROSITE; PS00041; HTF
Hypothetical protein.
SEQUENCE 761 AA; E
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01437; PSI; 1.
Pfam; PF01403; Sema; 1
SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-2002) to the EMBL; BC020974; AAH20974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WUA9
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000005; HTHAraC.
InterPro; IPR003659; Plexin-like.
InterPro; IPR003165; Plexin_repeat.
InterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical 83.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326
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                        FHEPG---
                                                                                                                             PPARLGLPL -- RLRLLLLLWAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVC-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYTSD---TVMQNPQFIKATIVHQDQAYD-DKIYYFFREDNPDKNPEAPLN----VSRVAQ
                                                                             PWSLLGLFLFQLLQLLLPTTTAGGGGQGPM---PRV----RYYAGDERRALS-----F 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRVEAEDG-TYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGRPVLVKT---HLAQQLHQIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q---QP-----IPTETFQVADRHPEVAQRVEPMGP----LKTPLFHSKYHYQKVAV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGVFSN---PWNYSAVCVYSLGDIDKVFR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCRGDQGGESSLSVSKWNTFLKAMLVCS---DAATNKNFNRLQDVFLLPDPSGQWRDTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALRSDSDQSLLHDPRFVMAARIPENSDQDNDKVYFFFSETVP--SPDGGSNHVTVSRVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQSCEPGHQSPNCI --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQDIRHGNPALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQSINPAEPHKECPNPKPDKAPLQKVSL----APNSRYYLSCPMESRHATYSWRHKENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSS----ERSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCVNDAGGQRVL-VNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAG--KSLEV
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                      PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                         83573 MW;
                                                                                                                                                                                                        14.3%;
SSSVWVGGRGKVYLFDF----PEGKN----ASVRTVNIGST 116
                                                                                                                                                                                   97;
                                                                                                                                                                                Score 516; DB 4
Pred. No. 7e-35;
97; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                         5BCB889AA32A2BB3
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annotation update)
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SEQUENCE FROM N.A.

MEDLINE=21082932; PubMed=11214970;

Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K.,

Prediction of the coding sequences of unidentified hur

Prediction of the coding sequences of unidentified hur

The complete sequences of 100 new cDNA clones from brai

for large proteins in vitro.";

DNA Res. 7:347-355(2000).

R EMBL; AB051256; BAB21830.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Plexin-like.

R InterPro; IPR003599; Plexin-like.
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O9COC4;
01-JUN-2001 (TrembLrel. 1
01-JUN-2001 (TrembLrel. 1
01-JUN-2002 (TrembLrel. 2
      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Primates;
Ig.
Ig_like.
Plexin-like.
Plexin_repeat.
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21,
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Last sequence update)
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                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
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SMART; SM00409;
SMART; SM00410;
SMART; SM00423;
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                                                                                                             Q9P2H9;
Q9P2H9;
                                 KIAA1368 protein (Fragment) KIAA1368.
                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
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   Eukaryota;
                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                              PNPKPDKAPLQKVSLAPNSRYYLSCPMESR--HATYSWRHKENVEQSCEPGHQSPNCILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCVYSLGDIDKVFRTSSLKGYHSS-----LPNPRPGKCL------PDQQPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSKWNTFLKAMLVCSDAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWN---YSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPQFIKATIVHQD----QAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDFLTLTLTEPTGLLY------VGAREALFAF-----SMEALELQGAISWEAPV
                                                                                                                                                                                                              PLENLGLVWLAVVALGAVCLVLLLLV
                                                                                                                                                                                                                                                                          DARLQALVVMAAQPRHAGAYHC
                                                                                                                                                                                                                                                                                                                                                                                                     MKY-RSCADCVLARDPYCAWSVNTSRCVAVGGHSGSLLIQHVMTSDTSG1CNLRGSKKVR
                                                                                                                                                                                                                                                                                                                                                                                                                          EVYGGGCHGCLMSRDPYCGW--DQGRCISIYSSERSVL-QSINPAEPHKEC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GWLLKAVSLGPWVHL----IEELQLFDQ-EPMRSLVLSQSKKLLFAGSRSQLVQLPVADC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNILNFVKKHPLMEEQVGPR--WSRPLLVKKGTNFTHLVADRVTGLDGATYTVLFIGTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TETFOVADRHPEVAQRVEPMGPLKTPLFHSK-YHYQKVAVHRMQASHGETFHVLYLTTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q-RKWTTFLKARLACSAPNWQLYFNQLQAMHTLQDTS--WHNTTFFGVFQAQWGDMYLSA
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                                                                                                                                                                                                                              -----LWLGVLP----TLTLGLLV
                                                                                                                                                                                                                                                                                                                                       PTPK-----
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   Metazoa;
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                                                                                                                            PRELIMINARY;
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); IG;
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Chordata;
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Last sequence update)
Last annotation updat
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   Craniata;
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   Vertebrata;
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   Euteleostomi;
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RESULT 13
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 Q9H2E6;
01-MAR-2001
                             Q9H2E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Prediction of the coding sequences of unidentified human The complete sequences of 150 new cDNA clones from brain v for large proteins in vitro.";

DNA Res. 7:65-73(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                               HLLDSPDSTDP
                                                                                                                                                                                                        GTIHK----VVEPGEQEHSFAFNIMEIQPFRRAA-----AIQTMSLDAERRKLYVSSQ 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PFSPDENSLVLFEGDEVYS-----TIRKQEYN--GKIPRFRRIRGESELYTSDTVM
                                                                                                                         HKENVEQSCEP
                                                                                                                                                     LGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSLLPSTTTSDSTAQEGYESRGGMLDWK
                                                                                                                                                                             -KECPN----PKPDKAPLQKV----SLAPNSRYYLSCPM---ESRHATYSWR
                                                                                                                                                                                                                                 WEVSQVPLDLCEVYGGGCHGCLMSRDPYCGW--DQGRCISIYSSERSVL-QSINPAEPH-
                                                                                                                                                                                                                                                             GIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFS
                                                                                                                                                                                                                                                                                                                 TLNFIKTHPLMDEAVPSI--FNRPWFLRTMVRYRLTKIAVDTAAGPY-QNHTVVFLGSEK
                                                                                                                                                                                                                                                                                                                                            TFQVADRHPEVAQRVEPMGPLKTPLF---HSKYHYQKVAVHRMQASHGETFHVLYLTTDR 433
                                                                                                                                                                                                                                                                                                                                                                       AYDMLDIASVF-TGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEPYFVQAV-----DYGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKW-----L
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  (TrEMBLrel.
                             PRELIMINARY;
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26.5%;
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Pred. No. 1.3e~28;
B; Mismatches 251
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                             1030
                             AA
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InterPro; IPR003659; Plexin-like.
InterPro; IPR001627; Sema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20564339; PubMed=10993894;
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                                                                                                                                                                                                                                                    388
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                                                                                                                                                       WEVSQVPLDLCEVYGGGCHGCLMSRDPYCGW--DQGRCISIYSSERSVL-QSINPAEPH-
DPLGAVSSHNHQDKKGVI 634
                              EP-----GHQSPNCIL 598
                                                             LGDCHN-----SFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDST
                                                                                                                                                                                     GIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFS
                                                                                                                                                                                                                    GTIHK----VVEPGEQEHSFAFNIMEIQPFRRAA-----AIQTMSLDAERRKLYVSSQ 482
                                                                                                                                                                                                                                                                                                              AYDMLDIASVF-TGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGSTKGSCLDKRDCENYI-TLLERRSEGLLACGTNARHPSCWNLVNGTVVPLG-EMRGYA 170
                                                                                          -KECPNPKPDKAPLQKVSLAPNSRYYLSCP-----MESRHATYSWRHKENVEQSC
                                                                                                                                                                                                                                                    TLNFIKTHPLMDEAVPSI--FNRPWFLRTMVRYRLTKIAVDTAAGPY-QNHTVVFLGSEK
                                                                                                                                                                                                                                                                                                                                                                           QWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRING--RDV-VLATFSTPYNSIPGSAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PFSPDENSLVLFEGDEVYS-----TIRKQEYN--GKIPRFRRIRGESELYTSDTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSRQAD 103
                                                                                                                          TCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDG
                                                                                                                                                                                                                                                                              TFQVADRHPEVAQRVEPMGPLKTPLF---HSKYHYQKVAVHRMQASHGETFHVLYLTTDR 433
                                                                                                                                                                                                                                                                                                                                           VYSLGDIDKVFRTSSLKGYHS------SLPNPRPGKC-----LPDQQPIPTE
                                                                                                                                                                                                                                                                                                                                                                                                       KWNTFLKAMLVCS-DAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNY---SAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                       KEPYFVQAV-----DYGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKW-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDTCRMKGKHKDECHNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEPG------RTVN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161;
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1030 AA;
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26.1%;
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Last annotation update)
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Pred. No. 5.4e-28;
0; Mismatches 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A57B79C10AEC4B34 CRC64;
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RESULT 15
Q9928
ID Q9928
AC Q9928
DT 01-QC
DT 01-JU
DE KIAA1
GN MEDLLI
RA MEDLLI
RA NAGAS
RT Which
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Best Local Sim
Matches 107;
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Q9P283;
Q1-OCT-2000 (TrEMBLrel. 15, C)
Q1-OCT-2000 (TrEMBLrel. 15, La
Q1-JUN-2002 (TrEMBLrel. 21, La
KIAA1445 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collapsin-2).";
collapsin-2).";
Submitted (MAY-2000) to the
EMBL; AF568594; AAFF6329.1;
ThterPro; IPR001627; Sema.
ThterPro; IPR01627; Sema.
 genes.
which
                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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Brenz Verca M.S., Widmer
"New rat semaphorin with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Semaphorin (Fragment).
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Q9JI29;
         SEQUENCE FROM N.A.

MEDLINE-20277482; pubMed-10819331;

Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human

genes.XVII.The complete sequences of 100 new cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                   KIAA1445
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                                                                                          NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVC----S
                                                                                                                                                                                                                                                                                                       DPY
                                                                                                                                                                                                                                                                                                                                                          MEEVVLEELQVFKHPTAILNMELSLKQQQLYVGSWDGLVQLSLHRCDTYGKACADCCLAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGPYAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIRRHPVMFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R------TSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVADRHPEVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGA-DTHFDELQDIYLLPT-----RDERNPVVYGVFTTTSSIFKGSAVCVYSIADIRAVF
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296 AA;
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Rodentia;
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closest
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Last annotation update)
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Sciurognathi; Muridae;
                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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 vitro.";
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avian Sema3D
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              from
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              brain
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Best Local
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SMART; SM00423;
SMART; SM00209;
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InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                     PNENLTERSLQDAQRLFLMSEAVQPVTP-EPCVTQDSVRFSHLVVDLVQAK-DTLYHVLX
                                                                                                                                                                                                                                                                                                                                          GESSLSVSKWNTFLKAMLVCS-DAATNKNFNRLQDVFLLPDPSGOWRDTRVYGVFSNPWN
                                                                                                                                                                                                                                                                                                                                                                                  YTSDTVMQNPQFIKATIVHQDQAYDDKIY-YFFREDNPDKNPEAPLNVSRVAQLCRGDQG
                                                                                                                                                                                                                                                                                                                                                                                                                      TTEKINGVARCPYDPRHNSTAVISSQGELYAATV--IDFSGRDPAIYRSLGSGPPLRTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVNIGS---TKGSCLDK----RDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --HPTVAFEDLQPWVSNFTYPGARDFSQLALDPSGNQLIVGARN--YLFRLSLANVSLLQ
NGAWTPWSSWALCSTSCGIGFQ
                         HATYS-WRHKENVEQSCEPGHQ
                                                   GGFGPWSPWQPCEHLDGDNSGSCLCRARSCDSPRPRCGGLD--CLGP-AIHIANC---SR
                                                                                                        VPLERCAAYRSQ-GACLGARDPYCGWDGKQQRCSTLEDSSNMSLWTQNITACPVRNVTRD
                                                                                                                                                          IGTESGTILKALSTASRSLHGCYLEELHVLPPGRREPLRSLRILHSARALFVGLRDGVLR
                                                                                                                                                                                  LTTDRGTIHKVVEPGEQE-HSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQ
                                                                                                                                                                                                                                   ----VADRHPEVAQR-----VEPMGPLKTPLFHSKYHYQKVAVHRMQASHGETFHVLY
                                                                                                                                                                                                                                                              SIAASAVCAFNLSAISQAF-----NGPFRYQENPR-AAWLPIANPIP--NFQCGTLPETG
                                                                                                                                                                                                                                                                                      ~--YSAVCVYSLGDIDKVFRTSSLKGYHSSLPNPRPGKCLPDQQPIPTETFQ------
                                                                                                                                                                                                                                                                                                                 GRELLE-DTWTTFMKARLNCSRPGEVPFYYNELQSAFHLPE-----QDLIYGVFTTNVN
                                                                                                                                                                                                                                                                                                                                                                     YNSKW-LNEPNFV-----AAYDIGLFAYFFLRENAVEHDCGRTVYSRVARVCKNDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                    LGE-MRGYA--PFSPDENS--LVLFEGDEVYSTIRKQEYNGKIPRFRRIRG-----ESEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGARTAEGPIMVLAGP---LAVSLLLPSLTLLVSHLSSSQDVSSEPSSEQQLCALSK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF01437; PSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB040878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 26.2
79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..J; Sema; 1
190; tsp_1; 5
23; PSI; 1
9; TSPI; 4
72; TSPI; 2
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1202 AA;
                                                                             PAEP-----HKECPNPKPDKAPLQKVSLAPNSRYYLSCPMESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAA95969.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %; Score 418; DB 4; L
%; Pred. No. 2.8e-26;
94; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1EF1FE8580953484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138;
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                                                                             571
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